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Mathematical framework for analyzing genome-wide association study data with rational classes

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Abstract

© 2014 by Nova Science Publishers, Inc. All rights reserved. Genome-wide association studies can statistically expose genes and biological processes involved in disease mechanics. Development of algorithms that increase the statistical power of genome-wide association studies remains an important research challenge. We present a mathematical approach to analyze a genome-wide association study. The method enables the use of Rational Classes to biologically direct the search for biomarkers and thus increase statistical power. Ranking of candidate biomarkers avoids the need for a Bonferroni-type correction. A modified q-value is introduced to provide a false-discovery rate type of measure in this setting